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Dev. Dyn. 218:102-111(2000).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                MEDLINE=98140125; PubMed=9479498;
                                                                                   TISSUE=Embryo
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                                                   "Identification of a novel RING finger protein as steroid receptor-mediated gene transcription."; mol. Cell. Biol. 18:5128-5139(1998).
-i- FUNCTION: ENHANCES STEROID RECEPTOR-MEDIATED
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Mammalia; Eutheria;
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Rattus norvegicus (Rat).
Purkarvota: Metazoa; Chordata;
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       ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION SUBUNIT: INTERACTS WITH GSCL, ANDROGEN RECEPTOR AND SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED PRIMARILY IN THE DEVELOPING NERVOUS SYSTEM MITH STRONG EXPERSION IN THE DORSAL ROOT GANGLIA AND GONADS. UBIQUITOUSLY EXPRESSED IN THE ADULT. DEVELOPMENTAL STAGE: EXPRESSION IS DETECTED FROM EMBRYONIC DAY AND CONTINUES THROUGHOUT DEVELOPMENT AND INTO ADULTHOOD. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear and cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: INTERACTS WITH GSCL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION AS WELL
                                                                                                                                                                                                                                                                                                                                           CPICMDGYSEIVQNGRLIVSTECGHVFCSQCLRDSLKNA--NTCPTCRKKI 184
                                                                                                                                                                                                                                                                                                                                                                   CTIC---
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(Rel. 40,
(Rel. 40,
                                                                                                                                                                                                                            protein 4 (SNURF).
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                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                             Poukka H.,
                                                                                                                                                                                Rodentia;
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                                                                                                             Karvonen
                                                                                                                                                                                                                                                                                                                                                                                        8;
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 1;
Pred. No. 7.6e-05;
                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                             Hakli M.,
                                                                                                                                                                                                                                                                                    B
                                            TRANSCRIPTION
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                                                                                       as
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                                                                                                             Janne O.A.,
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Best I
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Q02084;
Q1-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
2inc-binding protein A33.
Pleurodeles waltlii (Iberian ribbed newt).
Eukaryota; Metazoa; Chordata; Craniata; Verte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3H04; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A putative zinc-binding protein on lampbrush chromosome loops."; EMBO J. 12:107-114(1993).
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    EMBL; L04190; AAA49614.1;
                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93154311; PubMed=7679068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF022081; AAC35248.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.

BYMELOPMENTAL STAGE: IT FIRST APPEARS ON THE CHROMOSOME LOOPS AND IN THE NUCLEOPLASM OF THE GERMINAL VESICLE (GV). IT IS TRANSMITTED TO THE EGG AT GV BREAKDOWN AND APPEARS IN EMBRYONI NUCLEI AT THE MID-BLASTULA STAGE AND IS FOUND IN MANY BUT NOT ALL NUCLEI AT STILL LATER STAGES OF EMBRYOGENESIS.

SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

SIMILARITY: CONTAINS 1 BOX-TYPE ZINC FINGER.
                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: MAY BE A NUCLEAR REGULATORY PROTEIN THAT IS STORED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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194 AA;
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; 21896 MW;
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Pred. No. 7.66
8; Mismatches
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; 40C13970FC11DFF2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAPS_TORCA P09108;
                                                                                                                        SEQUENCE OF 8-412.

MEDLINE=88107644; PubMed=3427060;

Carr C., McCourt D., Cohen J.B.;

"The 43-kilodalton protein of Torpedo nicomembranes: purification and determination procedures are provided in the company of the control of the company of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                         Torpedo californica (Pacific electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                         Frail D.E., Mudd J., Shah V., Carr C., Cohen J.B., Mer "CDNAs for the postsynaptic 43-KDa protein of Torpedo encode two proteins with different carboxyl termini."; proc. Natl. Acad. Sci. U.S.A. 84:6302-6306(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
43 kDa receptor-associated protein of the synapse (RAPSYN)
(Acetylcholine receptor-associated 43 kDa protein) (43 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
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InterPro; IPR000315;
InterPro; IPR001841;
                                         MEDLINE=88331095; PubMed=3417776; Musil L.S., Carr C., Cohen J.B.,
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=87317641; Pubmed=3476945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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RNA-binding.
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"Acetylcholine receptor-associated bound myristate.";
                                                                                     MYRISTOYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    postsynaptic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00622; SPRY; 1.
PF000643; zf-B_box; 1.
PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SM00502; BBC; 1.
; SM00336; BBOX; 1.
; SM00184; RING; 1.
; SM00449; SPRY; 1.
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IPR003877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 10, Created)
(Rel. 15, Last seq
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Znf_bbox
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B BOX-TYPE.
COILED COIL.
SPRY.
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Pred. No. 0.00
13; Mismatches
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                                         Merlie
                        43K
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                                                                                                                                              nicotinic posts
                   protein
                                         J.P.;
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                                                                                                                                                                  postsynaptic
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                     covalently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                         Q9ULVB; Q9Y5Z3; Q9Y5Z2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Signal transduction protein CBL-C (SH3-bind
CBLC OR CBL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
PROSITE;
     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                    CBLC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PR00217; POSTSYNAPTIC.
ProDom; PD012428; Postsynaptic; 1.
SMART; SM000184; RING; 1.
SMART; SM00028; TPR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001237; Postsynaptic.
InterPro; IPR001440; TPR.
InterPro; IPR001441; Znf_ring.
Pfam; PF00515; TPR; 5.
Pfam; PF00097; Zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J02952; AAA49282.1; -. EMBL; J02953; AAA49283.1; -. PIR; A28009; A28009.
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-!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZN_FING
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                                                                                                                                                                                                                                                                                                                                                               362
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                                                                                                                                                                                                                                                                                                                                                        4 CTICSDFF-DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
| :| : | : | : | | | | | :| :| :| | | | :|
62 CGLCGESIGDQNSQLQALPCSHLFHLKCL----QTNGNRGCPNCK 402
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DOMAIN: A CYSTELNE-RICH RECION HOMOLOGOUS TO ART OF THE

REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN

INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.

SIMILARITY: BELONGS TO THE RAPSYN FAMILY.

SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.

SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO
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16; Conserv
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PS00518; ZF_RING_1; FALSE_NEG.
PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Postsynaptic membrane; Cytoskeleton; Phosphorylation; e; Zinc-finger; Alternative splicing.
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195
404
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361
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410
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195
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     Primates;
                            Chordata;
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PHOSPHORYLATION (POTENTIAL).
MISSING (IN SHORT ISOFORM).
Y -> T (IN REF. 2).
N -> D (IN REF. 2).
Y -> T (IN REF. 2).
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Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                 PRT;
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                                                                                                 tion update)
(SH3-binding
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  Hominidae;
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                                                                                                   protein CBL-C) (CBL-3).
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Best Local
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Pfam; PF02761; Cbl_N2; 1.
Pfam; PF02762; Cbl_N3; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00252; SH2; 1.
                          YQO9_CAEEL
Q09298;
Q1-NOV-1997
Q1-NOV-1997
16-OCT-2001
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: AB028645; BAA86298.1; -. EMBL; AF117646; AAD34341.1; -. EMBL; AF117647; AAD34342.1; -. HSSP; P22681; 1B47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00518; ZF_RING_1; 1. PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003153; Cbl_N.
InterPro; IPR000980; SH2.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penninger J., Lipkowitz S.; "cbl-3: a new mammalian cbl family protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Pancreatic adenocarcinoma; MEDLINE-99289203; PubMed-10362357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
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Kim M., Tezuka T., Suzuki Y., Sugano S., Hirai M., Yamamoto T.;
"Molecular cloning and characterization of a novel cbl-family gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keane M.M., Ettenberg S.A.,
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                                                                                                                                                                                                                                                            350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                           3 LCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
                                                                                                                                                                                                                                                         LCKICA---ESNKDVKIEPCGHLL-CSCCLAAWQHSDSQTCPFCRCEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239:145-154(1999).
                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                            Similarity 33...
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Zinc-finger; Phosphorylation; Alternative
89 92 NUCLEAR LOCALIZATION SIGNAL (F
(Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
1 141.2 kDa protein EEED8.9 in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 II
306 II
234 S
                                                                                                                                                                                                                                                                                                                                                                                 30.1%;
                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nau M.M., Banerjee P.,
                                                                                                                                                                                                                                                                                                                                                            Score 86; DB 1;
Pred. No. 0.0014;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RING-TYPE.
MISSING (IN SHORT ISOFORM).
T -> N (IN REF. 2).
; 91013DDF12828242 CRC64;
                                                                                                                                  1238
                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 474
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cuello
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Hypothetical

II.

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RAPSCLT RAPSCLT ID SCHOOL COLUMN COLU
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Z
ZN_FINC 908 945
DOMAIN 748 751
DOMAIN 124 1229
DOMAIN 1235 1238
SEQUENCE 1238 AA; 14
                                                                                                                                                                                                                                                                                                                                                                                                                               RAPS_CHICK
042393;
                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence
16-OCT-2001 (Rel. 40, Last annotati
43 kDa receptor-associated protein
(Acetylcholine receptor-associated
postsynaptic protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase; 2.
pfam; PF00097; zf-C3HC4; 1.
pfam; PF02148; zf-UBP; 1.
SMART; SM00184; RING; 1.
SMART; SM00290; ZnF_UBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U23484; AAC46769.1; -.
WormPep; EEED8.9; CE01893.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001841; Znf_ring.
InterPro; IPR001607; Zf-UBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases -:- SIMILARITY: TO YEAST YHLO10C AND S.POMBE SPAC16E8.1--:- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
Burns A.L., Benson D., Howard M.J., Marg
"Chick ciliary ganglion neurons contain
                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                 MEDLINE-97331014; PubMed-9185539;
                                                                                                  SEQUENCE
                                                                                                                                                                                          Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                             Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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751
1229
1238
                                                                                                                                                                                          Neognathae;
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                                                                                                                                                                                                                   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger.
KING-TYPE.
FOLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.
40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .98;
                                                                                                                                                                                                                                                                                                       sequence update)
annotation update)
protein of the synapse (RAPSYN)
sociated 43 kDa protein) (43 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86; DB Pred. No. 0.00 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-LYS
                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5B9A6E03AF91A703
                        Margiotta
                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
    transcripts
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0.0035;
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  coding for
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                                                                                                                                                                                        Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
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STITITE REPORTED THE REPORT OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKR3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local s
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001237; Postsynaptic.
InterPro; IPR001440; TPR.
InterPro; IPR001440; TPR.
InterPro; IPR001841; Snf_ring.
Pfam; PF00515; TPR; 6.
PRINTS; PR00217; POSTSYNAPTIC.
PRODOM; PD012428; POSTSYNAPTIC.
SMART; SM00184; RING; 1.
SMART; SM00028; TPR; 5.
                                                                                                                                                                                                                                                                Q60764;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
MAROTIN 3 (Zinc-finger protein 127).
MKRN3 OR ZEP127 OR ZNF127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetylcholine receptor-associated protein at synapses (rapsyn).";
J. Neurosci. 17:5016-5026(1997).
-i- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
THE NICOTINIC ACETYLCHOLLNE RECEPTOR AT SYNAPTIC SITES. IT MAY
LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
MEMBERANES.
Jong M.T.C., Carey A.H., Caldwell K.A., Lau M.H., Handel M.A., Driscoll D.J., Stewart C.L., Rinchik E.M., Nicholls R.D.; "Imprinting of a RING zinc-finger encoding gene in the mouse chromosome region homologous to the Prader-Willi syndrome genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT_MET
ZN_FING
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Synapse: Postsynaptic membrane; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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                                                                                                SEQUENCE FROM N...
PubMed=10196368;
                                                                                                                                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
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                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myristate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF000138; AAB63149.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MKR3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CTICSDFF-DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: EXPRESSED IN MUSCLE FIBERS AND IN NEUF DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE REGULATORY DOMAIN OF PROTEIN KINES C MAY BE IMPORTANT IN INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER. SIMILARITY: BELONGS TO THE RAPSYN FAMILY. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGMCGESIGEKNNQLQALPCSHFFHLKCL----QTNGTRGCPNCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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non-profit institutions as long
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                                                                                                                             N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402
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                                                                                                                                                                                                      Chordata;
Rodentia;
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Pred. No. 0.00
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
RING-TYPE.
MYRISTATE (BY SIMILARITY).
PHOSPHORYLATION (POTENTIAL);
851E7B2F4645B459 CRC64;
                                                                                                                                                                                                      Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                               on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    544
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                                                                                                                                                                                                                                Euteleostomi;
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                                                                                                                                                                                                           Murinae;
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Best Local S
Matches 18
                                                                     MEDLINE-970011/U; runned 3.

Buckel A., Beeson D., James M., Vincent A.;

Buckel A., Beeson D., James M., Vincent A.;

Cloning of cDNA encoding human rapsyn and mapping of the RAPSN gene locus to chromosome 11p11.2-p11.1.*;

Genomics 35:613-616(1996).

-i- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.

POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAPS_HUMAN STANDARD; PRT; 411 AA. 013702; 011-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 43 kDa receptor-associated protein of the synapse (Acetylcholine receptor-associated 43 kDa protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum.
                                                                                                                                                                                                                                                                                                                                       TISSUE-Muscle;
MEDLINE-97001170; PubMed-8812503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_C3H1; 3.
PROSITE; PS00518; ZF_RING_1;
PROSITE; PS50089; ZF_RING_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000571; zf-CCCH.
InterPro; IPR001841; znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF00642; zf-CCCH; 3.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              postsynaptic protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 VCGICMEVVYEKADPTDRRFGILFSCNHTYCLRCIRRWRSATQFENRISKSCPQCRVSSG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LCTICSDFFDHSRDVA-----AMDCGHTFHLQCL----IQSFETAPSRTCPQCRIQVG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . MO1. Genet. 8:795-803(1999).
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 3 C3H1-TYPE ZINC FINGERS.
                        DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE
     REGULATORY DOMAIN OF INTERACTIONS OF THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:99158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U19106; AAA76863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Similarity 30.(
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Repeat.
98 1
280 2
302 3
347 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
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298
329
401
456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.9%;
     PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C3H1-TYPE 1.
C3H1-TYPE 2.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85.5; Db 1;
Pred. No. 0.0018;
"" matches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FF05B7D034C5EA9F CRC64;
  KINASE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo
     TIPID
        BILAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 544;
                          PART OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RAPSYN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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RESULT 11
   В
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MEDLINE-88246464; PubMed-3380101;

A Takahashi M., Inaguma Y., Hiai H., Hirose F.;

A Takahashi M., Inaguma Y., Hiai H., Hirose F.;

A Takahashi M., Inaguma Y., Hiai H., Hirose F.;

T "Developmentally regulated expression of a human 'finger'-cont gene encoded by the 5' half of the ret transforming gene.";

Mol. Cell. Biol. 8:1853-1856(1988).

C -!- FUNCTION: MAY FUNCTION: Nuclear (Potential).

C -!- SUBCELLULAR LOCATION: Nuclear (Potential).

C -!- SUBCELLULAR LOCATION OF THE N-TERMINAL OF RFP WITH A PRO TYROSINE KINASE PRODUCES THE TRANSFORMING PROTEIN.

C -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

C -!- SIMILARITY: CONTAINS 1 BOX-TYPE ZINC FINGER.

C -!- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001440; TPR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00515; TPR; 5
PRINTS; PR00217; POSTSYNAPTIC.
ProDom; PD012428; POSTSYNAPTIC; 1
SMART; SM00184; RING; 1.
SMART; SM00028; TPR; 5
                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990
01-JAN-1990
01-MAR-2002
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00405; 43-KD_POSTSYNAPTIC; PROSITE; PS00518; ZF_RING_1; FALSE_NEG PROSITE; PS50089; ZF_RING_2; 1.
Synapse; Postsynaptic membrane; Cytoska
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                       RFP_HUMAN P14373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPID
                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                        Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myristate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 CALCGESIGEKNSRLQALPCSHIFHLRCL----QNNGTRSCPNCR 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTICSDFF-DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR
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0 0
362 402
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(Rel. 13, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                      protein RFP (Ret finger protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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195 P
404 P
46199 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Postsynaptic TPR.
is copyright. It is produced through a collaboration stitute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84.5; D
Pred. No. 0.00
10; Mismatches
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MYRISTATE
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PHOSPHORYLATION (POTENTIAL)
6A9FBA4B95E58CBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.5; DB 1
No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                     513
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                                                                                                                                                                                           e F.;
a human 'finger'-containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                PROTEIN
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Best Local
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Interpro: IPR003878; SPRY_dom
Interpro: IPR00315; Znf_bbox
Interpro: IPR001841; Znf_ring
pfam; PF00622; SPRY; 1.
Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-G3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _MOUSE MOUSE STANDARD; PRT; 411 AA P12672; 01-OCT-1989 (Rel. 12, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 43 kDa receptor-associated protein of the s (Acetylcholine receptor-associated 43 kDa p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZN_FING
ZN_FING
DOMAIN
SEQUENCE
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SMART; SM00336; BBOX; 1.
SMART; SM00134; RING; 1.
SMART; SM001449; SPRY; 1.
PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS50119; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
PROSITE; PS50089; ZF_RING_2; Metal-binding; Chromosomal translocation; Nuclear protein; DNA-binding.
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MEDLINE=89008468; PubMed=3170600; Frail D.E., McLaughlin L.L., Mudd J., Merlie J.P.; "Identification of the mouse muscle 43,000-dalton receptor-associated protein (RAPsyn) by cDNA cloni
                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                             Froenner S.C.;
"Expression of RNA transcripts for the innervated and denervated rat skeletal FEBS Lett. 249:229-233(1989).
                                                                                                                                                                                                                                  Froehner S.C.
                                                                                                                                                                                                                                                     MEDLINE=89289985; PubMed=2737281;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                            RAPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               postsynaptic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L; J03407; AAA365; A28101; TVHURF.; 602165; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPVCLQYF - - - AEPMMLDCGHNICCACLARCWGTAETNVSCPQCR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSR-TCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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96
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127
493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Znf_bbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPRY_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gamma_carbxylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFP-RET ONCOGENE.
RING-TYPE.
B BOX-TYPE.
SPRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84; DB
Pred. No. 0.00
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BREAKPOINT FOR TRANSLOCATION TO FORM THE
                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6F963D9048D8A731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
the synapse (RAPSYN)
kDa protein) (43 kDa
                                                                                                                                                                                    postsynaptic 43
muscle.";
    cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 513;
                          acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                       Murinae;
                                                                                                                                                                                                            kDa
                                                                                                                                                                                                       protein
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Best Local S
Matches 15
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Interpro; IPR001237; Postsynaptic.
Interpro; IPR001240; TPR.
Interpro; IPR001841; 2nf_ring.
Pfam; PF00515; TPR; 6.
PRINTS; PR00217; POSTSYNAPTIC.
PRODOm; PD012428; POSTSYNAPTIC; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
SMART; SM0028; TPR; 3.
PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.
PROSITE; PS0018; ZF_RING_1; FALSE_NEG.
PROSITE; PS0089; ZF_RING_2; 1.
Synapse; POSTSYNAPTIC membrane; Cytoskele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 263:15602-15607(1988).

-i- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
                                                                                                         01-NOV-1997 (
01-NOV-1997 (
16-OCT-2001 (
Hypothetical
                                                                                                                                                               YQ57_CAEEL
Q09463;
                                                                                                                                                                                             _CAEEL
                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myristate; INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF TH
REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT
INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
-i- SIMILARITY: BELONGS TO THE RAPSYN FAMILY.
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                    Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                             ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
 SEQUENCE FROM N.A. STRAIN-BRISTOL N2
                                       NCBI_TaxID=6239;
                                                                               Caenorhabditis elegans
                                                                                               C16C10.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                362 CGLCGESIGERNSRLQALPCSHIFHLRCL----QNNGTRSCPNCR 402
                                                                                                                                                                                                                                                                          4 CTICSDEF-DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S04488; S04488.
A31995; A31995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X15788; CAA33789.1;
J03962; AAA40030.1;
                                                                                                                                                                                                                                                                                                    ch 29.2%;
l Similarity 33.3%;
15; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                   ; Zinc-finger.
0 0
362 402
1 1
195 195
404 404
343 344
                                                                                                                                                                                                                                                                                                                                                                        411 AA;
                                                                                                            (Rel.
(Rel.
1 24.9
                                                                                                                                                 (Rel.
                                                                                                                                                                             STANDARD;
                                                                                                          35,
35,
40,
kDa
                                                                                                                                                                                                                                                                                                                                                                        46233 MW;
                                                      Nematoda; Chromadorea; inae; Caenorhabditis.
                                                                                                         Last sequence update)
Last annotation update)
protein C16C10.7 in chr
                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .
                                                                                                                                                                                                                                                                                                      10;
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MYRISTATE.

PHOSPHORYLATION (POTENTIAL PHOSPHORYLATION (POTENTIAL DV -> EL (IN REF. 2).

DV -> EL (IN REF. 2).

DV -> EL (IN REF. 2).
                                                                                                                                                                                                                                                                                                  Score 83.5; DB 1
Pred. No. 0.0025;
0; Mismatches 1
                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoskeleton; Phosphorylation;
                                                                                                                                                                             235
                                                                                                                                                                             A
                                                                                                            chromosome
                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                    Rhabditida; Rhabditoidea,
                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                               Length 411;
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                                                                                                            III
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
 entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                        Q06003;
01-FEB-1994
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                               Goliath protein (G1 protein).
GOL OR G1 OR GL.
Drosophila melanogaster (Fruit fly)
         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                         Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                    "The Drosophila melanogaster developmental gene zinc-finger-motif protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000306; Znf_FYVE.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                   between
                                                                                                                                   ++
                                                                                                                                                                                                                               Bouchard M.L., Cote
                                                                                                                                                                                                                                           MEDLINE=93216124; PubMed=8462875;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                               Ephydroidea;
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOLI_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical 
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00064; FYVE; 1
SMART; SM00184; RING; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; C16C10.7; CE01498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 246787; CAA86745.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lloyd C.;
Submitted (NOV-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAP-SRTCPQCR 47
                                                                                                                                 e 125:205-209(1993).

FUNCTION: REGULATION OF GENE EXPRESSIC PUTATIVE ROLE AS TRANSCRIPTION FACTOR. SUBCELLULAR LOCATION: Nuclear.

TISSUE SPECIFICITY: VISCERAL MESODERM
                                                                                                         SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS
                                                                                                                       MUSCULATURE.
                                                                SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNIC---LDAAKDAVVSLCGHLFCWPCLSQWLDTRPNNQVCPVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00518; ZF_RING_1; PS50089; ZF_RING_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
235 #
                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 28, Created)
(Rel. 28, Last seq
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein; Zinc-finger
26 67 RING
121 124 POLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                             Drosophilidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
 ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 F
124 F
172 F
24915 MW;
                                                                                                                                                                                                                                                                                                             Endopterygota; Diptera;
ilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.0%;
37.8%;
                                                                                                                                                                                                                                                                                                                                                                                            Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 83; DB
Pred. No. 0.00
6; Mismatches
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POLY-ALA.
; 21A04AE951F6382A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                   MESODERM AND
                                                                                                                                                                         EXPRESSION DURING MESODERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                284
                                                                                                                                                                                                                                                                                                                                                                                          update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
.0017;
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                                                                                                                                                                                                                                                                                                                       Brachycera; Muscomorpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                  PRIMORDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 235;
                                                               and the
                                                                                                                                                                                                                 g1 encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                   S,
                                                                   EMBL
                                                                   a collaboration
                                                                                                                                                                                                                 a variant
                                                                                                                                   SOMATIC
                                                                                                                                                                           FORMATION
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Best Local S
Matches 16
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Pfam; PF00097; zf-C3HC4; 1.

SMART; SM00184; RING; 1.

SMO0184; RING; 1.

SMO0184; RING; 1.

SMO0185; zF_RING_1; FALSE_NEG.

PROSITE; PS00518; zF_RING_2; 1.

Developmental protein; Zinc-finger; Transcription regulation; Dayelopmental protein; Zinc-finger; Transcription regulation; DNA-binding; Nuclear protein.

ZN_FING 126 167 RING-TYPE.

DOMAIN 208 259 GLN/PRO/SER-RICH.

DOMAIN 208 259 GLN/PRO/SER-RICH.

SEQUENCE 284 AA; 31973 MW; ECEE2D5EEDBA1E2B CRC64;
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed the companies of the companies of the contract of the companies o
                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: DETECTED IN MOST ORGAN LEVELS IN THYMUS, HEART, BRAIN AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-91249381; van Lohuiizen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haupt Y., Alexander W.S., Barri G., Kl
"Novel zinc finger gene implicated as
retrovirally accelerated lymphomagenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-91249382; PubMed-1904009;
MEDLINE-91249382; PubMed-1904009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel.
01-MAY-1992 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                            -!- DISEASE: COOPERATES WITH THE MYC ONCOGENE TO -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by provirus tagging.";
Cell 65:737-752(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 65:753-761(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BMI1_MOUSE 
P25916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0004919; gol.
                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of cooperating oncogenes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gulden H., Berns A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BMI1 OR BMI-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polycomb complex protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 CAICIEAYKPTDTIRILPCKHEFHKNCIDPWLIE-----HRTCPMCKLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED IN ITS EXPRESSIBILITY.
                                                                                                                                                                                                                                                                                                                                                               (PCG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Verbbeek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22, Created)
22, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1904008;
Verbbeek S., Scheijen B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.7%;
31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Barri G., Klinken S.P., Adams J implicated as myc collaborator by lymphomagenesis in E mu-myc trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BMI - 1
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.0027;
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use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).

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P35226; Q96F37;
01-FEB-1994 (Rel. 28, C
01-FEB-1994 (Rel. 28, I
01-MAR-2002 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hum.
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TISSUE-Erythrocyte;
MEDLINE-94093545; PubMed-8268912;
MICHARD A.K
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PROSITE; PS50089; ZF_RING_2; 1.
Chromatin regulator; Nuclear protein; T
Repressor; Zinc-finger; Proto-oncogene.
ZN_FING 18 57 RING-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                    European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed. Ities requires a license agreement (See send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
DISEASE: COOPERATES WITH THE MYC ONCOGENE TO SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN ITS EXPRESSIBILITY SUBUNIT: COMPONENT OF
                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Swiss Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content.
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      BC011652;
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complex protein BMI-1.
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324 AA;
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                                       AAA19873.1;
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      AAH11652.1;
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324 P
36707 MW;
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Primates;
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Pred. No. 0.00
L3; Mismatches
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NUCLEAR LOCALIZATION SIGNAL
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( InterPro; IPR001841; 2..._

R Pfam; PP00097; zf-C3HC4; 1.

R SMART; SM00184; RING; 1

DR PROSITE; PS000518; Zf_RING_1; 1.

DR PROSITE; PS50089; ZF_RING_1; 1.

DR Chromatin regulator; Nuclear protein; Transcription regenerates and the second seco
RESULT 17
ME18_MOUSE
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
DNA-binding protein Mel-18.
ZNF144 OR ZFP144 OR ZFP-144 OR MEL18 OR MEL
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SEQUENCE
                                                                                                                                                                                                                                                                    MEDLINE=91060627; PubMed=2246278; Tagawa M., Sakamoto T., Shigemoto K., MaIto T., Nakamura I., Okitsu A., Imai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96091139;
                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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Biol. Chem. 26
                                                                                                       IN NEURAL TISSUES.

DEVELOPMENTALL STAGE: DEVELOPMENTALLY REGULATE
DISCASE: PROBABLY RELATED TO TUMORGENESIS SIN
STRONGLY IN MOST TUMOR CELL LINES.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: EXPRESSED
                                                                                                                                                                                                                                                  CELL DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCVLCGGYFIDATTI--IECLHSFCKTCIVRYLET--SKYCPICDVQV
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15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ovel DNA-binding protein with zinc cells.";
                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8521824;
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326 P
265 V
36935 MW;
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31.2%;
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Best Local
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              between
the Euro
                                                                                                                                                                      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS SPECIFICALLY TO THE DNA SEQUENCE 5'GACTNGACT-3'. HAS A TUMOR SUPPRESSOR ACTIVITY. MAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _HUMAN
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or send a
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ZNF144 OR MEL18
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01-FEB-1994 (Rel.
                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                        TISSUE-Placenta;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          Taniguchi M., Kanno M.;
"Cloning and chromosome mapping encodes a DNA-binding protein w. Gene 129:249-255(1993).
                                                                                                                                                                                                                                                                                                                                                                       Ishida A., Asano H.,
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-93314969;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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16-OCT-2001
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D90085; BAA14122.1; -
EMBL; BC016419; AAH16419.1;
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                                                                         SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: DETECTED IN ALL TISSUE EX
EXPRESSION FOUND IN PLACENTA LUNG AND KIDNEY
IN LIVER, PANCREAS AND SKELETAL MUSCLE.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                  European Bioinformatics Institute.
              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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PS0089; ZE_RING_2; 1.
ption regulation; Repressor; Zinc-finger; DNA-binding; protein; Phosphorylation.

18 57 RING-TYPE.
18 95 NUCLEAR LOCALIZATION SIGNAL (POTE 242 342 PRO/SER-RICH.
237 237 PHOSPHORYLATION (BY CAPK)
                                                                                                                                                              DEVELOPMENT
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40,
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H., Hasegawa M.,
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license@isb-sib.ch).
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29.2%;
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Last
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C23031B8B9E30108 CRC64;
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Catarrhini;
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Zinc-finger;

Repeat. 96 1: 125 1:

C3H1-TYPE

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MKR4_HUMAN
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Best Local S
Matches 14
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; Zf-C3HC4; I.
Pfam; PF00642; Zf-CCCH; 4.
SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_C3H1; 4.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS00589; ZF_RING_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat)
Makorin 4 (Zinc-finger protein 127-Xp) (ZNF
MKRN4 OR ZNF127L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               escapes X chromosome inactivation.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGERS.
-i- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                InterPro; IPR000571;
InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Hendrich B.D., Longstreet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKR4_HUMAN
Q13434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00518; ZF_RING_1; 1. PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00097; zf-C3HC4; SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 600346;
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                                                                                                                                                                               EMBL; U41315; AAA99070.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "An X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willard H.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homologue of the autosomal imprinted gene ZNF127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JN0717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344
37788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.7%;
29.2%;
                                                                                                                                                             Zf-CCCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₹,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82; DB 1;
Pred. No. 0.0032;
4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR LOCALIZATION SIGNAL PRO/SER-RICH.
A910BCD4C0CE9927 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gustashaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
) (2NF127-Xp).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicholls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 21
Z173_HUMAN
ID Z173_H
AC Q12899
DT 16-OCT
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YP99_CA
                                                                                      Вþ
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FT
FT
FT
                                                                                                                                                Query Match
Best Local Similarity
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16-OCT-2001 (Rel. 40
Hypothetical 22.7 kD
C28H8.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                              InterPro; IPR001965; PHD.
InterPro; IPR001961; Znf_ring.
InterPro; IPR001841; Znf_ring.
Pf00628; PHD; 2.
SMART; SM00249; PHD; 2.
SMART; SM00184; RING; 1.
Hypothetical protein; Zinc-finger; Nuclear proteing B6 12 PHD-TYPE 1.
ZN_FING 143 191 PHD-TYPE 2.
SEQUENCE 202 AA; 22725 MW; F627355EB73AD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YP99_CAEEL
Q09477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZN_FING
DOMAIN
ZN_FING
ZN_FING
SEQUENCE
Z173_HUMAN STANDARD;
Q12899;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller N., Waterston R.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Nuclear (Potential).
-i- SIMILARITY: BELONGS TO THE REQUIEM/D4 FAMILY.
-i- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                          WormPep; C28H8.9; CE06896.
                                                                                                                                                                                                                                                                                                                       EMBL; U20861; AAA62297.1; -.
                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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                                                                                      144
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                                                                                                     CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAP--SRTCPQCRIQVG
                                                                                      CTICGTSENDDKLLFCDDCDRGYHLYCLTPALEKAPDDEYSCRLCQVEFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCGICMEVVYEKANPNEHRFGILS-NCNHTFCLKCIRKWRSAKEFESRIVKSCPQCRI
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18; Conservative
                                                                                                                                     16;
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271
316
405
485
                                                                                                                                    Conservative
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298
370
425
52909 .
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40,
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2. Last sequence update)
0. Last annotation update
0. Tost annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.5%;
                                                                                                                                               28.3%;
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MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
C3H1-TYPE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 81.5; Di
Pred. No. 0.00
12; Mismatches
                                                                                                                                    9;
                                                                                                                                    Score 81; DB Pred. No. 0.00 9; Mismatches
                                                                                                                                                                                                PHD-TYPE 1.
PHD-TYPE 2.
; F627355EB73AD26A
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                          539
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in chromosome
                                                                                                                                               DB 1;
.0026;
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                                                                                                                                                           Length 202
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                                                                                                                                    Indels
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                                                                                                                                    Gaps
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RESULT 22
2147_MOUSE
ID 2147_MOUSE
AC Q61510;
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                                                                                                                        Query Match
Best Local S
Matches 17
                                                                                                                                                                                                          PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS50119; ZF_RING_1; FJ
PROSITE; PS50089; ZF_RING_2; 1
Zinc-finger; Coiled coil.
ZN_FING 16 57
ZN_FING 97 138
DOMAIN 188 227
DOMAIN 365 539
SDOMAIN 388 400
P
                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Chu T.W., Capossela A., Coleman R.
"Cloning of a new 'finger' protein
region of the human MHC.";
Genomics 29:229-239(1995).
                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00622; SPRY; 1.
Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003878;
InterPro; IPR000315;
InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01406; BBOXZNFINGER SMART; SM00336; BBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                       SMART;
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                                                                         16
                                                                                                4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSR-TCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600830;
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                                                                         CSICLDYL --
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SM00449; SPRY;
                                                                                                                          Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A
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                                                                                                                                                                                       422
539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein 173 (Acid
                                                                                                                          Conservative
                                                                                                                                                                                       AA;
             STANDARD;
                                                                         -RDPVTIDCGHVFCRSCTTDVRPISGSRPVCPLCK
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62165 MW;
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Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gamma_carbxylse.
                                                                                                                                     28.3%;
37.8%;
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protein gene (ZNF173) within the
                                                                                                                        5.
                                                                                                                        Score 81; DB Pred. No. 0.005; Mismatches
                                                                                                                                                                                                            RING-TYPE.
B BOX-TYPE.
COILED COIL
SPRY.
POLY-GLU.
                                                                                                                                                                                      POLY-GLU.
842A71C41F2E2348 CRC64;
                                                                                                                                                                                                                                                                                                    FALSE_NEG
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             PRT;
             634
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                                                                                                                          19;
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                                                                                                                                               Length 539
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RESULT 23
CBL_HUAN
ID _CBL_H O1-AU
AC P2268
DT 01-AU
DT 16-OC
DE Signa
GN CBL C
OS HOMO
OC EUKAI
OC Mamma
OX NCBI [1]
RN [1]
RP SEQUE
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR003877; SPRY.
InterPro: IPR003878; SPRY.domain.
InterPro: IPR001841; Znf_ring.
InterPro: IPR001841; Znf_ring.
Pfam; PF00622; SPRY: 1.
Pfam; PF00062; SPRY: 1.
SMART; SM00184; RIMG; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                       CBL_HUMAN STANDARD;
P22681;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content than the swing and the swing as its content to the swing 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA in target organs.";
J. Biol. Chem. 270:24406-24413(1995).
-i- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-i- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
                                                                                                                                            Signal transduction CBL OR CBL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Zinc finger protein 147 (Estrogen responsive finger protein) (Efp).
ZNF147 OR ZFP147 OR EFP.
                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00518; ZF_RING_1; PROSITE; PS50089; ZF_RING_2; Zinc-finger; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:102749; LLPLT..
InterPro; IPR001870; Gamma_carbxylse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orimo A., Inoue S., Ikeda K., Noji S., Muramatsu M.;
"Molecular cloning, structure, and expression of mouse estrogen-
responsive finger protein Efp. Co-localization with estrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Uterus, Ovary, and Placenta; MEDLINE-96025835; PubMed-7592654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFET-APSRTCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                 CSVCLELF --
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15; Conser
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305
631
71772
                                                                      Chordata;
Primates;
                                                                                                                                                                   protein
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33.3%;
                                                                                                                                                                                            Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                   CBL
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Pred. No. 0.00
8; Mismatches
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COILED COIL (POTENTIAL).
SPRY.
; 6695C9DE2832E611 CRC64;
                                                                 Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                   (Proto-oncogene
                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                         906
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.0078;
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                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                   c-CBL).
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                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
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RESULT 24
YOUD_CAEEL

AC AC

P30631;

YOUD_CAEEL

STANDARD;

PRT;

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Best Local
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InterPro: IPR001841; Znf_ring.
Pfam; PF02262; Cbl_w; 1.
Pfam; PF02761; Cbl_W2; 1.
Pfam; PF02762; Cbl_W3; 1.
Pfam; PF002762; Cbl_W3; 1.
Pfam; PF00627; UBA; 1.
Pfam; PF00097; Zf-C3HC4; 1.
                                                                                                                                                                                                                        DOMAIN
DOMAIN
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MOD_RES
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 47-350.

**MEDLINE-99176421; PubMed=10078535;

Meng W., Sawasdikosol S., Burakoff S.J., Eck M.J.;

**Structure of the amino-terminal domain of Cbl complexed to its binding site on ZAP-70 kinase.";

Nature 398.84-90(1999).

-i- FUNCTION: PARTICIPATES IN SIGNAL TRANSDUCTION IN HEMATOPOIETIC CELLS. ADAPTOR PROTEIN THAT FUNCTIONS AS A NEGATIVE REGULATOR (MANY SIGNALLING PATHWAYS THAT START FROM RECEPTORS AT THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequences of the human and mouse c-obl proto-oncogenes show v-obl was generated by a large truncation encompassing a proline-rich domain and a leucine zipper-like motif."; Oncogene 6:653-657(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00184; RING; SMART; SM00165; UBA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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-!- SIMILARITY: CONTAINS 1 UBA DOMAIN.
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380
                                            3 LCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATED ON TYROSINE
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LCKICA---ENDKDVKIEPCGHLMCTSCL-TSWQESEGQGCPFCRCEI
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1B47; 27-APR-99
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                                                                                                16;
                                                                                                                       Similarity
                                                                                                                                                                                                                             906
                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein; Zinc-finger; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZF_RING_1;
ZF_RING_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2030914;
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420
476
688
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700
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                                                                                             10;
                                                                                                                       Score 80; DB 1;
Pred. No. 0.015;
                                                                                                                                                                                                                        PHOSPHORYLATION.
PHOSPHORYLATION.
7D686B050204AD8F CRC64;
                                                                                                                                                                                                                                                                                                                                                  ASP/GLU-RICH PRO-RICH.
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UBA.
                                                                                                                                                                                                                                                                                                                                                                                                    RING-TYPE
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                                                                                                Mismatches
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                                                                                                                                            DB 1;
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                                                                                                                                            Length 906
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RESULT 25
2179_HUMAN
ID 2179, HUMAN
AC Q9ULXS; 0600
DT 16-OCT-2001
DT 16-OCT-2001
DT 01-MAR-2002
DE Zinc finger
GN ZNF179 OR BI
OS Homo sapien
OC Eukaryota; 1
OC Mammalia; E:
OX NCBI_TaxID=0
RN [1]
RP SEQUENCE FR
RA Seki N., Ha
RT "Human BFP/
RL Submitted (
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Best Local
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16-OCT-2001 (Rel. 4
Hypothetical 18.8 kt
ZK637.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z11115; CAA77447.1; -.

PIR; S15788; S15788.

Wormbep; ZKG37.14; CE00432.

InterPro; IPR001841; Znf_ring.

Pfam; PF00097; zf-C3HC4; 1.

SMART; SM00184; RING; 1.

PROSITE; PS00518; ZE_RING_1; FALSE_NEG.

PROSITE; PS50089; ZF_RING_2; 1.
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Peloderinae; Caenorhabditis.
                                                                                                                                  Q9ULX5; O60633;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
Zinc finger protein 179 (Brain finger prote
ZNF179 OR BFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear S., Cou Craxton M., Durbin R.K., Berks M., Metzstein M., Hawkins T., Ainscough R., Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Zinc-finger.
ZN_FING 72 134 RING-
SEQUENCE 161 AA; 18847 MW; F5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92168156; PubMed=1538779; Sulston J., Du Z., Thomas K., Wilson R.,
                 SEQUENCE FROM N.A.
Seki N., Hattori A.,
"Human BFP/ZNF179.";
                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
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                                                                            NCBI_TaxID=9606
                                                                                                                          Homo sapiens (Human)
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kDa
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Primates;
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protein ZK637.14 in chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 79.5; DB 1;
Pred. No. 0.0032;
; Mismatches 22;
                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                PRT;
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protein)
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Best Local
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01-NOV-1995
01-NOV-1995
16-OCT-2001
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 146.8 kDa protein C34E10.5 in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB026054; EMBL; AF054587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: Predominantly expressed -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            finger protein (bfp), a me Genomics 33:325-327(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96301415; PubMed≈8660987; Matsuda Y., Inoue S., Seki N., Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE OF 33-127 FROM N.A.
EMBL; U10402; AAA19067.1; -
WormPep; C34E10.5; CE01185.
InterPro; IPR001841; Znf_ri
                                                                                                                                                                    -i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-i- SIMILARITY: TO S.POMBE SKB1 AND YEAST YBR133C
                                                                                                                                                                                                                             Kirsten
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00518; ZF_RING_1; PROSITE; PS50089; ZF_RING_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 601237;
                                                                                                                                                                                                             Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                      C34E10.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger.
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Chromosome mapping of human (ZNF179), finger protein (bfp), a member of the I
                                                                                                                                                                                                                                                                                                                                                                                                                                         YLB5_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 CSIC---LERLRDPISLDCGHDFCIRC----FSTHRLPGCEPPCCPECR
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632 AA;
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68354 MW;
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Pred. No. 0.014;
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RING finger
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PROSITE: PS50089; ZF KI
PROSITE: PS50089; ZF KI
Hypothetical protein: T
Hypothetical protein: T
TRANSMEM 69 89
F TRANSMEM 1165 1185
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Best Local
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                                                Pfam; PF00622; SPRY; 1.
Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-C3HC4; 1.
PRINTS; PR01406; BBOXZNFINGER.
SMART; SM00336; BBOX; 1.
SMART; SM00346; RING; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ULT 27
                                                                                                                                          Interpro; IPR003877; Interpro; IPR003878; Interpro; IPR003815; Interpro; IPR000315; Interpro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          062158;
01-NOV-1997 (Rel. 35, Created
01-NOV-1997 (Rel. 35, Last se
01-MAR-2002 (Rel. 41, Last an
Zinc-finger protein RFP (Ret
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
PROSITE; PS50119; ZF_BBOX; 1.

PROSITE; PS00518; ZF_RING_1; 1.

PROSITE; PS50089; ZF_RING_2; 1.

Zinc-finger; Metal-binding; Nuclear protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97176437; PubMed=9023983;
Cao T., Shannon M., Handel M.A., Etkin L.D.;
"Mouse ret finger protein (rfp) proto-oncogene
specific stages of mouse spermatogenesis.";
Dev. Genet. 19:309-320(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
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Mammalia; Eutheria;
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                                                                                                                                                                                              MGD; MGI:97904; Rfp. InterPro; IPR001870;
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                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                              FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVE
SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER
SIMILARITY: CONTAINS 1 SPRY DOMAIN.
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                                                                                                                                                                                                                       L46855; AAA85354.1;
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; SM00184; RING; 1.
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16; Conserv
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1185
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Rodentia;
                                                                                                                                                        ; SPRY_domain.
; Znf_bbox.
                                                                                                                                                                                                                                                       Latement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                        Znf_ring.
                                                                                                                                                                                            Gamma_carbxylse.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                            a collaboration
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RESULT 28
STE5_YEAST
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P32917;
01-OCT-1993
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ZN_FING
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                  SEQUENCE
Mackay V.
                                                                                                                                                                                                                                                                                                                             MEDLINE-93296161; PubMed-8516289; Perlman R., Yablonski D., Simchen G., Levitzki A.; "Cloning of the STE5 gene of Saccharomyces cerevisiae as a suppressor of the mating defect of cdc25 temperature-sensitive mutants."; proc. Natl. Acad. Sci. U.S.A. 90:5474-5478(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                   Mukai Y., Harashima S., Oshima Y.;
"Function of the ste signal transduction pathw
pheromones sustains MAT alpha 1 transcription
cerevisiae.";
                                                                         STRAIN-S28BC / AB972:

Murphy L., Harris D., Barrell B.G., Rajandream M.A.;

Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

SUBMITTED: COMPONENT OF THE PHEROMONE SIGNAL TRANSDUCTION PATHWAY

IT MEDIATES PHEROMONE SIGNALS ACTING BETWEEN STE20 AND STE11.

IT IS ABSOLUTELY REQUIRED FOR PHEROMONE-INDUCED TRANSCRIPTION OF FUS1. MAY PLAY A ROLE IN CELL-CYCLE ARREST IN RESPONSE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
           ÷
                                                                                                                                                                                        protein kinase to Farl.";
                                                                                                                                                                                                                                                                                                                                                                                                            MOL.
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STE5 OR NUL3 OR YDR103W OR
                                                                                                                                                                                                           "Cloning
                                                                                                                                                                                                                        Thomas D.Y
                                                                                                                                                                                                                                            MEDLINE=94067004;
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STRAIN=DBY939;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=93296161;
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01-OCT-1996
                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                  Leberer
                                                                                                                                                                                                                                                                                        Submitted
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                             PHEROMONE.
SUBCELLULAR LOCATION: Cytopl
PTM: MAY BE REGULATED AT THE
MATING TYPE OF THE CELL AND
          RESPONSE PATE SIMILARITY:
                                                                                                                                                                            Gen.
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28,
34,
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                                                     Cytoplasmic
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B BOX-TYPE.
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Pred.
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DEPENDS ON AN INTACT PH
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Ste5
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                                                                                                                           "Cloning and characterization of cbl-b: a SH3 binding pr
homology to the c-obl proto-oncogene.";
L Oncogene 10:3367-3277 (1995).
C -!- SUBUNIT: INTERACTS WITH SH3 DOMAIN PROTEINS FYN, FGF
C -!- SUBCELIULAR LOCATION: Nuclear (Potential).
C -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A LONG FORM (SHOWN
TRUNCATED ISOFORM 1 AND TRUNCATED ISOFORM 2; ARE PRO
ALTERNATIVE SPLICING.
C -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, KIDNEY, SPLEE
AS WELL AS FETAL BRAIN AND LIVER AND HEMATOPOIETIC C
AND IN ADULT BRAIN, LIVER, PANCREAS, SALIVARY GLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.9%;
Best Local Similarity 30.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    _HUMAN
CBLB_HUMAN STANDARD; PRT; ybz nn.
(D13191; Q13192; Q13193;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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EMBL;
PIR; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGD;
                                            This
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
               the
                           between the
                                                                                                                                                                                                                                                                                               Keane M.M., Rivero-Lezcano Lipkowitz S.;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=95303504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pheromone
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BL; L01620; AAA35115.1; -.

BL; L02865; AAA35115.1; -.

BL; L07865; AAA16896.1; -.

BL; 247746; CAA87679.1; -.

R; S30810; S30810.

R; S30920; S39920.

D; S0002510; STE5.

D; S0002510; STE5.

ART; SM001841; Znf_ring.

ART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ν
                                                                  PTM: PHOSPHORYLATED ON TYROSINES.
SIMILARITY: CONTAINS 1 RING-TYPE Z
SIMILARITY: CONTAINS 1 UBA DOMAIN.
               European
          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASCTLCDEPISNRRKGEKITELACGHLSHQECLITSFGTTSKADVRALFPFCTKCK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALCTICSDFFDHSR----DVAAMDCGHTFHLQCLIQSFETAPSRT------CPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response.
775
331
341
341
821
917 AA;
                                                                                                                                                                                                                                                                                                           PubMed=7784085;
o-Lezcano O.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                876
332
343
821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77; DB
Pred. No. 0.03
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASP/GLU-RICH (ACIDIC).

LG -> W (IN REF. 2).

NSI -> TLS (IN REF. 2).

A -> R (IN REF. 1).

A; 0435BDA0196B2D6F CRC64;
                                                                                                                                                                                                                                                                                                           Mitchell J.A., Robbins K.C.,
                                                                                      ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
0.036;
                                                                                                                             G, KIDNEY, SPLEEN, AND TESTIS, HEMATOPOIETIC CELL LINES, BUT SALIVARY GLAND, OR SKELETAL
                                                                                      FINGER
                                                                                                                                                                                                                                                                               binding
                                                                                                                                                                                                                                                                                                                                                                                                                                               protein CBL-B)
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                                                                                                                                                                                                        (SHOWN
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                                                                                                                                                                                                                                                                              protein
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Best Local S
Matches 15
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InterPro; IPR000449; UBA.
InterPro; IPR0001841; Znf_ring.
InterPro; IPR001841; Znf_ring.
Pfam; PF02262; Cbl_N; 1.
Pfam; PF02762; Cbl_N3; 1.
Pfam; PF02762; Cbl_N3; 1.
Pfam; PF00627; UBA; 1.
Pfam; PF000627; UBA; 1.
SMART; SM00184; RING; 1.
SMART; SM00185; UBA; 1.
SMART; SM00185; UBA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
VARSPLIC
VARSPLIC
VARSPLIC
SEQUENCE
          MEDLINE=20499367; PubMed=11042152; Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G. Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G. Zhang J.-Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-Y., Tao J., Chen Z., Chen Z., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z., "Cloning and functional analysis of cDNAs with open reading frames 300 previously undefined genes expressed in CD34+ hematopoietic
                                                                                                                                          SEQUENCE FROM N.A.

MEDILINE=21481893; PubMed=11597136;

MEDILINE=21481893; PubMed=11597136;

MID A., Abe S., Nicholls

Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls

"Phylogenetic conservation of the makorin-2 gene, encoding

zinc-finger protein, antisense to the rafl proto-oncogene."

Genomics 77:119-126(2001).
                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                  MKR2_HUMAN STANDARD; PRT; 416 AA Q9H000; Q9NRY1; Q9BUY2; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat makerin 2 (HSPC070).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U26710; AAB09291.1; -.
EMBL; U26711; AAB09292.1; -.
EMBL; U26712; AAB09293.1; -.
HSSP; P22681; 1B47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not remove
entities requires a license agreement (So
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 604491;
                                                                                                  SEQUENCE FROM N.A. TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00518; ZF_RING_1; 1. PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003153; InterPro; IPR000980;
                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                           MKRN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 LCKICA---ENDKDVKIEPCGHLMCTSCL-TAWQESDGQGCPFCRCEI 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV
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N 116 119 NUCLEAR LOCALIZATION

NG 373 412

RING-TYPE.

N 477 701 PRO-RICH.

N 931 970 UBA.

PLIC 812 982 MISSING (IN TRUNCATE

LIC 767 770 DVFD -> TYRI (IN TRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 26.9%;
l Similarity 31.2%;
15; Conservative
undefined r cells.";
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412
701
970
982
770
982
109479
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SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Score 77; DB
8; Pred. No. 0.03
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW; 038D4965DAFB98CB CRC64;
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DVFD -> TYRI (IN TRUNCATED ISO
MISSING (IN TRUNCATED ISOFORM
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PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1
つ.038;
                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                               Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                                                                                                                                       R.D.;
n multiple
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MKR2_M
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Best Local
                                                                                                                                                                                                                                Matches
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InterPro; IPRO01841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF000642; zf-CCCH; 4.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS00518; ZF_RING_2; 1.
                                                                                         ULT 31
2_MOUSE STANDARD
09ERV1; Q9DOL9;
01-MAR-2002 (Rel. 41, C
01-MAR-2002 (Rel. 41, L
01-MAR-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                     ZN_FING
ZN_FING
DOMAIN
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                  CONFLICT
                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                       MKRN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome
 MEDLINE-21481893; PubMed-11597136
          SEQUENCE FROM N.A.
                             NCBI_TaxID=10090;
                                                                                  Makorin
                                                                                                                                                                                                                                                                                                                                                                   Zinc-finger;
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF
TISSUE-Eye;
                                                                                                                                                                                      237 VCSICMEVILEKASASERRFGILSNCNHTYCLSCIRQWRCAKQFENPIIKSCPECRV
                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitted (JAN-2001) to the EMBL/GenBank/DDBJ databases TISSUE SPECIFICITY: Widely expressed.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                                                                           LCTICSDFF-----DHSRDVAAMDCGHTFHLQCLIQ-----SFETAPSRTCPQCRI
                                                                                                                                                                                                                                         Similarity
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171
193
238
238
327
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                               Repeat.
                                                                                                                                                                                                                                                                                  A,
                                                                                                                                    STANDARD;
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189
222
292
347
186
278
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28
                                                                                           Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                        3.18;
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                                                                                                                                                                                                                                                                             RING-TYPE.
C3H1-TYPE 4.
F -> V (IN REF. 2 AND 3).
K -> E (IN REF. 2).
O2B6B7A8BD38ZDDC CRC64;
                                                                                                                                                                                                                             Score 76.5; D
Pred. No. 0.01
LO; Mismatches
                                                                                                                                                                                                                                                                                                                                   C3H1-TYPE 1.
C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                     PRT;
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RESULT 32
TTC3_HUMAN
ID TTC3_HUMAN
                                                                                                   DЬ
                                                                                                                                                                                                                                                                           Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batahov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batahov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl R., Catulli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,
A Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Blake J., Bult D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Havashiyaki Y., Storch K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Havashiyaki Y., Storch K., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1914277; Mkrn2.
InterPro; IPRO00571; Zf-CCCH.
InterPro; IPRO01841; Znf_ring.
Pfam; PF00097; Zf-C3HC4; 1.
Pfam; PF00642; Zf-CCCH; 4.
SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_C3H1; 4.
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ZN_FING
CONFLICT
SEQUENCE
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ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF277171; AAG27596.1; -. EMBL; AK011295; BAB27523.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA Nature 409:685-690(2001).
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-Embryo; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                            ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
                                                                                                   237
                                                                                                                                                                                             Local
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                                                                                                   VCSICMEVILEKASASERREGILSNCSHTYCLSCIRQWRCAKQFENPIIKSCPECRV
                                                                                                                                                                           l Similarity
16; Conserv
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                                                                                                                                                                                             26.7%;
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
L -> F (IN REF. 2).
L -> F (SOURCE CRC64;
                                                                                                                                                                           Score 76.5; D
Pred. No. 0.01
10; Mismatches
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                                                                                                                                                                                             DB 1;
).019;
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ZN_FING
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Metazoa; Chordata;
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tetratricopeptide repeat protein 3 (TPR repeat
                                                                                                                                                                                                                                    Pfam; PF00515; TPR; 4.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsukahara F., Hattori M., Muraki T., Sakaki Y.; "Identification and cloning of a novel cDNA belonging to tetratricopeptide repeat gene family from Down syndrome-critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
DNA Res. 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96281123;
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Mammalia; Eutheria;
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InterPro; IPR001841; Znf_ring.
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Tsukahara F., Hatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a novel human gene containing the tetratricopeptide repeat domain from the Down syndrome region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagase T., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohira M., Ootsuyama A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain;
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: 3 ISOFORMS; TRPDI (SHOW AND TPROIII; SEEMS TO BE PRODUCED BY ALTERNATISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAM SIMILARITY: CONTAINS 4 TPR REPEATS.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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SM00028; TPR; 3.
E; PS00518; ZF_RING_1;
E; PS50089; ZF_RING_2;
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                                     % repeat;
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     Ä,
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ma A., Suzuki E.,
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      229889
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ARG/LYS-RICH (BASIC).
ARG/LYS-RICH (BASIC).
ARG/LYS-RICH (BASIC).
ARG/LYS-RICH (BASIC).
ARG/LYS-RICH (BASIC).
MISSING (IN ISOFORM TPRDIII).
MISSING (IN ISOFORM TPRDIII).
MW: 1B4BCAA3684B6253 CRC64;
                                                                                                               TPR 2.
TPR 3.
TPR 4.
RING-TYPE.
                                                                            POLY-SER.
POLY-LYS.
POLY-LYS.
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Best Local Similarity
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                                                                                         Pfam; PR00622; SPRY; 1.
Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-C3HG4; 1.
PRINTS; PR01406; BBOXZNFINGER.
SMART; SM00136; BBOX; 1.
SMART; SM00184; RING; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
16-OCT-2001 (Rel.
                                                            PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Macrophage;
MEDLINE-96215393; PubMed-8625517;
Keech C.L., Gordon T.P., McCluskey J.;
"Structural differences between the human and autoantigens associated with poorly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1957
                                                                                                                                                                                                                      MGD;
                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
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                     DOMAIN
                                        ZN_FING
                                                  Zinc-finger;
                                                                                                                                                                            InterPro; IPR000315;
                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                   InterPro; IPR001841;
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                                                                                                                                                                                                                     MGI:106657;
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                                                             PS50119;
PS00518;
PS50089;
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IPR001870; Gamma_carbxylse.
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   Antigen;
20 59
96 12
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470 AA;
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127
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54175 1
                                                          ; ZF_BBOX; 1.
; ZF_RING_1; 1.
; ZF_RING_2; 1.
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36, Last
40, Last
1 (Sjogren
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Rodentia;
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znf_bbox.
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                                      RNA-binding; Ribonucleoprotein; RING-TYPE.
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            MW.
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annotation update)
syndrome type A antigen
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Pred. No. 0.12
7; Mismatches
                    B BOX-TYPE.
LEUCINE-ZIPPER
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          393AE5AFD254855B CRC64;
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autoantibody
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; Murinae; Mus
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                                                   DNA-binding
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Best Local
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YQ55_CAEEL

Q09251;
01-NOV-1997 ()
01-NOV-1997 ()
01-NCV-1997 ()
Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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770418;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Zinc finger protein 179 (Brain finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
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pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inoue S., Orimo A., Saito T.,
Ouchi Y., Muramatsu M.;
"A novel RING finger protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=98042506;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chem. Biophys. Res. Commun. 240:8-14(1997).
TISSUE SPECIFICITY: Predominantly expressed in brain.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                    CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPS---RTCPQCR
                                                                                                                                                                                                                                                                                                           CSIC---LERLREPISLDCGHDFCIRCF--STHRIPGCELPCCPECR
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16; Conserv
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                                                                                                                                                                                                    STANDARD;
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40,
kDa
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68646
                      Nematoda;
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34.0%;
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    Caenorhabditis.
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Pred. No. 0.04
8; Mismatches
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                        Rhabditida;
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                        Rhabditoidea;
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                                                                                                                      Macropus eugenii (Tammar wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Diprotodontia; Macropodidae; N
MCBI_TaxID=9315;
                                                                                                                                                                         Makorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
         -!- SIMILARITY:
                            "The ancient source of a distinct gene famile featuring RING and C(3)H zinc-finger motifs in developing brain and nervous system."; Genomics 66:76-86(2000).
                                                                                        SEQUENCE FROM N.A.
MEDLINE=20304755; PubMed=10843807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z46787; CAA86743.1; -. WormPep; C16C10.5; CE01496. InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                 MKRN1
                                                                                                                                                                                                                   Q9TT91;
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RING; 1.

18; ZF_RING_1; FA.

0089; ZF_RING_2; 1

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21 protein; Transme
296 358

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17; Conser
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        RING-TYPE
C3H1-TYPE
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Pred. No. 0.04
8; Mismatches
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                                                                      Smithwick M.J
R.D.;
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01-MAR-2002 (Rel. 4
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SEQUENCE
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                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF192786; AAF17489.1; ...
InterPro; IPR001395; Aldo_ket_red.
InterPro; IPR000571; Zf-CCCH.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                         MEDLINE=20304755; PubMed=10843807;
Gray T.A., Hernandez L., Carrey A.H., Schaldach M.A., Smith
Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
"The ancient source of a distinct gene family encoding profeaturing RING and C(3)H zinc-finger motifs with abundant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
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Pfam; PF00642; zf-CCCH; 4.
                                                                                                                                                                     in developing brain and nervous system.", Genomics 66:76-86(2000).
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch).
                                                                                                                                           SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER. SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
            ; AF192785; AAF17488.1; -.
MGI:1859353; Mkrn1.
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SM00356; ZnF_C3H1; 4.
E; PS00518; ZF_RING_1;
E; PS50089; ZF_RING_2;
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57
86 1
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478 AA;
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
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Matches 16
                                                                                                                           Genome Res. 11:422-435(2001).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                              Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Gl
Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Straok
Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heu
Wambutt R., Korn B., Klein M., Poustka A.;
"Towards a catalog of human genes and proteins: sequencin
analysis of 500 novel complete protein coding human cDNAs
Genome Res. 11:422-435(2001).
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DOMAIN
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ZN_FING
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Pfam; PF00097; zf-C3HC4;
Pfam; PF00642; zf-CCCH; 4
                                                                                                                                                                                                                                                                                                                                                                                  Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Rus K., Marshall Graves J.A., Stewart C.L., Nicholls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UHC7; Q9UEZ7; Q9H0G0;
01-MAR-2002 (Rel. 41, C
01-MAR-2002 (Rel. 41, L
01-MAR-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_C3H1; 4.
                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                               Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00518; ZF_RING_1; PROSITE; PS50089; ZF_RING_2;
EMBL; AF192784; AAF17487.1;
                                                                                                                                                                                                                                                                            MEDLINE=21154917; PubMed=11230166;
                                                                                                                                                                                                                                                                                        TISSUE=Testis
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               in developing brain and Genomics 66:76-86(2000).
                                                                                                                                                                                                                                                                                                                                                        "The ancient source of a distinct gene family encoding proteins featuring RING and C(3)H zinc-finger motifs with abundant expression
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=20304755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Makorin
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16; Conservative
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Primates;
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28.1%;
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annotation update)
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE 4.
C3H1-TYPE 4.
C3H1-TYPE 4.
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7. 0.052;
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                                   http://www.isb-sib
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; Zf-C3C4; 1.
Pfam; PF00642; Zf-CCCH; 4.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS00518; ZF_RING_2; 1.
PROSITE; PS00518; ZF_RING_2; 1.
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01-FEB-1995 (Rel. 3
16-OCT-2001 (Rel. 4
Hypothetical 67.5 )
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                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
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SEQUENCE
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VARIANT
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Vignati D., Wilcox L.,
                                                                                                                                                                                 Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      YEAST
                                                                                                           Science 265:2077-2082(1994).
-!- SIMILARITY: TO C.ELEGANS EEED8.9
                                                                                                                                                                                                                                                STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                                                                -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                 "Complete nucleotide sequence
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Eukaryota; Fungi; Ascomycota; Saccharomyc
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, AF192789; AAF18979.1;

, AF192790; AAF18979.1;

, AF192791; AAF18979.1;

, AF192792; AAF18979.1;

, AL136812; CAB66746.1;

, AL136812; CAB66746.1;
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 license@isb-sib.ch).
          license agreement (See http://www.isb-sib.
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28.1%;
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Pred. No. 0.05
L1; Mismatches
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C3H1-TYPE 4
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                                                                                                           AND S. POMBE
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                       nt is in no way and for commercial
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Best Local
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Interpro; IPR001841; Znf_ring.

Interpro; IPR001607; zf-UBP.
Pfam; PF00099; zf-C3HC4; 1.
Pfam; PF00184; Znf_UBP; 1.
SMART; SM00184; RING; 1.
SMART; SM00290; ZnF_UBP; 1.
SMART; SM00290; ZnF_UBP; 1.
PROSITE; PS000518; ZF_RING_1; FALSE_PROSITE; PS00089; ZF_RING_2; 1.
Hypothetical protein; Zinc-finger.
ZN_FING 240 280 RING-T
SEQUENCE 585 AA; 67503 MW; 88FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
RING finger protein 12 (LIM domain interacting
(RING finger LIM domain-binding protein) (R-I.TM
RNF12 OR RLIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9WTV7;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                               entities
or send a
                   EMBL; AF069992; Ar
MGD; MGI:1342291;
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                  factors via recruitment of the histone deacety.
Nat. Genet. 22:394-399(1999)
-i- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR I
TRANSCRIPTION FACTORS. VIA THE RECRUITMENT
DEACETYLASE COREPRESSOR COMPLEX.
-i- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTOR-
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGI
                                                                                                                                                                                                                                                                            MEDLINE=99364422; PubMed=10431247;
Bach I., Rodriguez-Esteban C., Carriere C.,
Rose D.W., Glass C.K., Andersen B., Izpisua
Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                         "Opposing developmental functions of positive coregulators of LIM homeodomain factors."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
PIR;
                                                                          modified and this statement is not removed entities requires a license agreement (See
                                                                                                     the European Bioinformatics Institute. The By non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                              "RLIM inhibits functional activity of LIM
                                                                                                                                                                                                                                                                                                                                   FUNCTION
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                                     AF069992; AAD34209.1; -.
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an email to license@isb-sib.ch).
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6; Mismatches
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Sciurognathi; Muridae,
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